What's next in now-gen sequencing.

The Illumina® Genome Analyzer.

illumina®

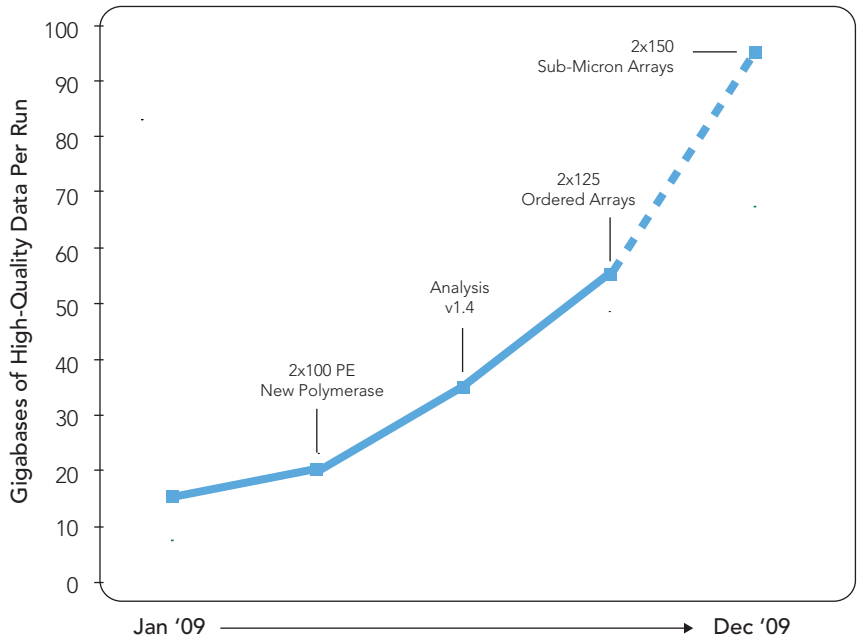
Expect more from your sequencer.

Not just more data, **better data.**

With the Genome Analyzer, we've moved beyond the next generation of sequencing. Now-Gen sequencing is a dedication to continuous improvement: enhanced analysis, simplified workflow. A commitment to innovation. A devotion to helping you publish faster. A promise to improve upon the best data quality available today.

In 2008, the Genome Analyzer saw a 15-fold increase in output. What can you expect for 2009? Higher output. Lower cost per project. Superior quality with enhanced analysis. And access to a broader set of applications and simpler experimental designs than you thought possible.

Raise your expectations. Join the Illumina Community.

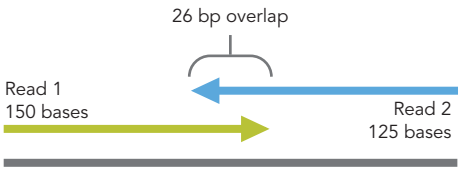


Anticipated 2009 System Improvements.

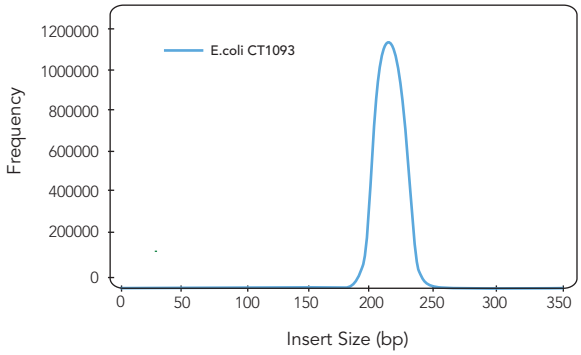
Register for our upcoming webinars at www.illumina.com/sequencing

Read length, **extended.**

- Combination of short-insert libraries and long reads enables overlap reads extending beyond 250 bases.
- Contiguous reads of 250 bases simplify *de novo* sequencing, metagenomics, and targeted resequencing applications.
- For each application of interest, select the optimal combination of read length (from 2 x 17 to greater than 2 x 100) and pair separation (200 bp to 5 kb).



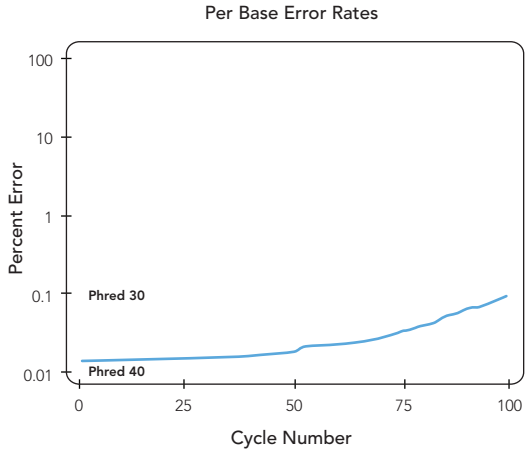
Standard Paired-End Library



Insert Size Distribution

Data quality, **unmatched.**

- Enhanced analysis and new algorithms produce more than 70% Q30 bases per run for 2 x 75 bp reads.
- New cluster generation enzyme and other enhancements increase percentage of Q30 and Q40 bases.
- Improved data quality enhances SNP calling, variant detection, and polymorphism confirmation.



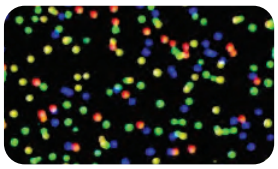
Run completed in January 2009 with GA_{IIx} configuration and new enzyme and polymerase.

Simple workflow, **made simpler.**

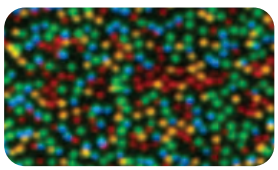
- Larger reagent cooler enables walk-away automation for up to 125 cycles of sequencing.
- ≥ 2 x75 base pair reads eliminate the need for concatenation and shearing steps in targeted sequencing. Save time, save starting material, and increase your yield.
- Streamlined reagent kits simplify the workflow, require fewer reagents, minimize manual steps, and reduce set-up time.

Data density, (more than) **tripled.**

- Demonstrated image analysis improvements increase output of reads per run by greater than 80% (from Pipeline 1.0 to Pipeline 1.4).
- Ordered arrays using 1.0 micron features potentially double the output of high-quality data.
- Reducing feature size to sub-micron levels will further increase output.



Random Array Clusters



Semi-ordered Array

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